

10/585964 SEQ ID NO:24

Db 61 GIFIETKGLWDSSDRKKHLLIREQHPELDIRLVFSSSRSKLYKGSPTSYGEWCEKHGILF 120
 Qy 121 ADKLIPAEWIKEPKKEVPPDRLKRKGKK 149
 ||||| :|||||||: |||||
 Db 121 ADKLIPVAGVKEPKKEVPPDRLKRKGVK 149

10/585964 SEQ ID NO:25

RESULT 12
 ENRN_BPT3
 ID ENRN_BPT3 Reviewed; 152 AA.
 AC P20314;
 DT 01-FEB-1991, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1991, sequence version 1.
 DT 25-NOV-2008, entry version 38.
 DE RecName: Full-Endodeoxyribonuclease I;
 DE EC=3.1.21.2;
 DE AltName: Full-Endodeoxyribonuclease I;
 DE Short-Endonuclease;
 GN Name=3;
 OS Enterobacteria phage T3 (Bacteriophage T3).
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
 OC Autographivirinae; T7-like viruses.
 OX NCBI_TaxID=10759;
 OH NCBI_TaxID=562; Escherichia coli.
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=Luria;
 RX MEDLINE=90133923; PubMed=2614843; DOI=10.1016/0022-2836(89)90102-2;
 RA Beck P.J., Gonzalez S., Ward C.L., Molineux I.J.;
 RT "Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.";
 RL J. Mol. Biol. 210:687-701(1989).
 CC --!- FUNCTION: Endodeoxyribonuclease I, which is expressed in the late stage, is necessary for T3 genetic recombination and the breakdown of host DNA. In the early stage of infection, T3 DNA replicates as a linear monomer. In the late stage, the T3 DNA replicates via linear concatemers several genomes in length. The gene 3 product has also been implicated in the maturation of these concatemers.
 CC --!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-phosphooligonucleotide end-products.
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 DR EMBL; X17255; CAA35132.1; -; Genomic_DNA.
 DR PIR; S07505; S07505.
 DR RefSeq; NP_523312.1; -.
 DR RNSP; P00641; IMOD.
 DR SMR; P20314; 17-145.
 DR GeneID; 927412; -.
 DR GO; GO:0005634; Cinnucleus; IEA:InterPro.
 DR GO; GO:0008833; Fid:Endodeoxyribonuclease IV (phage-T4-induced) act. . .; IEA:InterPro.
 DR GO; GO:0003677; Fid:DNA binding; IEA:InterPro.
 DR GO; GO:0015074; Fid:DNA integration; IEA:InterPro.
 DR GO; GO:0016032; Piviral reproduction; IEA:InterPro.
 DR InterPro; IPR008029; Endonuclease_I_phage.
 DR InterPro; IPR011578; Restrict_endonuc_C/endonuc_I.
 DR Gene3D; G3DSA:13.40.91.30; Restrict_endonuc_C/endonuc_I; 1.
 DR Pfam; PF05367; Phage_endo_I; 1.
 PE 4; Predicted;
 KW Endonuclease; Hydrolase; Nuclease.
 FT CHAIN 1 152 Endodeoxyribonuclease 1.
 FT . /FTId=PRO_0000106485.
 SQ SEQUENCE 152 AA; 17432 MW; BFCDE82A4C0D61B CRC64;
 Query Match 77.2%; Score 615; DB 1; Length 152;
 Best Local Similarity 83.1%; Pred. No. 5.6e-49;
 Matches 113; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 14 AFRSCLEDKVSKQLESKGIKFYEYEEWKVYVIAASNHTYTPDFLLPNGIEVETKGLWESD 73
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
DB 14 AFRSCLEDKVSKQLESKGIKFYEYEEWKVYVIAASNHTYTPDFLLPNGIEVETKGLWESD 73
QY 74 DRKKHILLIREQHPELDIIRVFSSSRTKLYKGSPTSYGEFCEKHGIKFADKLIPAEWIKEP 133
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
DB 74 DRKKHILLIREQHPELDIIRVFSSSRSKLYKGSPTSYGEWCEKHGILFADKLIPVAGVKEP 133
QY 134 KKEVSPFDRLKRKGCGKK 149
|||:|||:|||:
DB 134 KKEVSPFDRLKRKGCGKK 149